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(54) Title: COMPOUNDS THAT BIND TO p185 AND METHODS OF USING THE SAME (57) Abstract Novel peptides and pharmaceutical compositions comprising the same are disclosed. Conjugated compositions peptides linked to detectable agents and/or cytotoxic agents are disclosed. Method of detecting tumors that have p185 on tumor cell surfaces are disclosed. Methods of preventing transformation of a normal cell into a tumor cell in an individual at risk of developing a tumor having tumor cells which have p185 on their surfaces are disclosed. Methods of treating an individual who has cancer characterized by tumor cells that have a p185 on their cell surfaces are disclosed.		

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COMPOUNDS THAT BIND TO p185 AND METHODS OF USING THE SAME**FIELD OF THE INVENTION**

The invention relates to compounds useful for and methods of treating individuals suspected of suffering from tumors and preventing tumors in individuals suspected of being susceptible to the development of tumors and for detecting and imaging tumors.

BACKGROUND OF THE INVENTION

Significant amounts of time and money have been spent to better understand cancer and searching for ways to prevent and cure cancer. The results of these research efforts have provided a greater understanding of the biological and biochemical events that participate in the formation of tumors.

Malignant cells display a variety of characteristics that distinguish them from normal cells. Recent studies in the molecular genetics of cancer indicate that certain genes known as oncogenes may play a role in the transformation of some cells from their normal condition to a cancerous condition. Proto-oncogenes, genes closely related to these genes, are found in somatic cells of all eukaryotic species examined and have been highly conserved in evolution; it is thought that proto-oncogenes normally play critical roles in cellular growth and development. Oncogene amplification and chromosomal rearrangements involving oncogenes have been detected in a large number of tumors. Furthermore some tumors have been shown to contain activated oncogenes which, in DNA transfection assays, are capable of conferring neoplastic properties upon non-neoplastic rodent fibroblast cell lines. Collectively

- 2 -

these studies suggest that alterations in proto-oncogene structure and function play a critical role in the development of neoplasia.

Although most oncogene-encoded proteins reside in the nucleus or the cytoplasm, some oncogenes encode proteins that are present as antigenic sites on the cell surface. For example, the *erbB-1*, *erbB-2*, *erbB-3*, *erbB-4*, *fms* and *ros* oncogene products are transmembrane glycoproteins that possess extracellular domains. The *sis* oncogene product may also exist in a membrane associated form on the surface of transformed cells.

Another oncogene which encodes a protein that exposes antigenic sites on the surface of transformed cells has been identified by transfection of DNA from ethyl nitrosourea-induced rat neuroblastomas into NIH3T3 cells. This oncogene has been termed *neu*. The homologous human gene is called *erbB-2*. The *erbB-2* gene has been found to be amplified or overexpressed in some human tumors, particularly those of the breast, suggesting that this gene may play an important role in the etiology of human cancer.

The protein encoded by the *erbB-2* oncogene is a 185kDa transmembrane glycoprotein with tyrosine kinase activity, generally known by the name p185. The *erbB-2* gene is closely related to the epidermal growth factor (EGF) receptor gene in structure.

The *erbB-2* oncogene and p185 has also been found active in human adenocarcinomas including breast, lung, salivary gland and kidney adenocarcinomas, as well as prostate neuroblastoma. In human primary breast cancers, amplification of the *erbB-2* oncogene was found in about 30% of all malignant tumors examined. Increased stage of malignancy, characterized by large tumor size and increased number of positive lymph nodes as well as reduced survival time and decreased time to relapse, was directly correlated with an increased level of amplification of the *erbB-2* gene. The *erbB-2* protooncogene is expressed at low levels in normal human tissues. Further, *erbB-2* has been associated with 100% of the ductal carcinomas

- 3 -

studied *in situ*, Lodato, R.F., et al. (1990) *Modern Pathol.* 3(4):449.

Current treatments for individuals suffering from carcinomas expressing amplified levels of *erbB-2* include surgery, radiation therapy, chemotherapy, immunotherapy and, usually, combinations of two or more of such therapies. Despite advances made in these fields, the mortality rate among individuals suffering from cancer remains unacceptably high. Complete tumor eradication and total remission is not always the outcome.

There remains a need for additional modalities in the anti-tumor approaches and for additional methods of reducing and/or eliminating tumors in individuals. There is a need for anti-tumor agents which can be administered as therapeutics to individuals suffering from tumors, particularly tumors with amplified levels of *p185*.

While changes in diet and behavior can reduce the likelihood of developing cancer, it has been found that some individuals have a higher risk of developing cancer than others. Further, those individuals who have already developed cancer and who have been effectively treated face a risk of relapse and recurrence.

Advancements in the understanding of genetics and developments in technology as well as epidemiology allow for the determination of probability and risk assessment an individual has for developing cancer. Using family health histories and/or genetic screening, it is possible to estimate the probability that a particular individual has for developing certain types of cancer. Those individuals that have been identified as being predisposed to developing a particular form of cancer can take only limited prophylactic steps towards reducing the risk of cancer. There is no currently available method or composition which can chemically intervene with the development of cancer and reduce the probability a high risk individual will develop cancer.

Similarly, those individuals who have already developed cancer and who have been treated to remove the cancer

- 4 -

or are otherwise in remission are particularly susceptible to relapse and reoccurrence. As part of a treatment regimen, such individuals can be immunized against the cancer that they have been diagnosed as having had in order to combat a recurrence.

- 5 Thus, once it is known that an individual has had a type of cancer and is at risk of a relapse, they can be immunized in order to prepare their immune system to combat any future appearance of the cancer.

There is a need for improved preventative agents for
10 individual with a high risk to develop cancer and for individuals who have had cancer enter remission or be removed. In cases where the type of cancer the individual is at risk to develop, such as tumors associated with erbB-2, there is a need for specific agents which can be administered to reduce the
15 probability that a predisposed individual will develop cancer or that a patient in remission will suffer a relapse.

There is a need for therapeutic compositions useful to treat individuals identified as having p185-associated tumors. There is a need to develop prophylactic compositions
20 for individuals susceptible to developing p185-associated tumors.

SUMMARY OF THE INVENTION

The present invention relates to peptides having the formula:

25 $R_1 - R_2 - R_3 - R_4 - R_5 - R_6 - R_7$

wherein:

R_1 is 1-6 amino acid residues and at least one of which is tyrosine or phenylalanine;

R_2 is a linking moiety which bonds with R_1 ,
30 R_3 and R_6 such that a portion of said peptide is cyclicized;

R_3 is 0-20 amino acids;

R_4 is 6 amino acids;

R_5 is 0-20 amino acids;

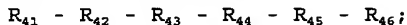
R_6 is a linking moiety which bonds with R_5 ,
35 R_7 and R_2 such that a portion of said peptide is cyclicized;

- 5 -

R_7 is 1-6 amino acid residues and at least one of which is tyrosine or phenylalanine;

wherein: R_1 , R_2 , R_3 , R_4 , R_5 , R_6 and R_7 , taken together, are 30 amino acids or less;

5 and R_4 is has the formula:



wherein:

either,

10 R_{41} is E or D;

R_{42} is N or Q;

R_{43} is W;

R_{44} is D or E;

R_{45} is W; and,

R_{46} is Y or F;

15 or

R_{41} is G, V, A, I or L;

R_{42} is D or E;

R_{43} is G, V, A, I or L;

R_{44} is F or Y;

20 R_{45} is Y or F; and,

R_{46} is A, I, L, G or V.

The present invention relates to conjugated compositions that comprise such peptides linked to detectable agents and/or cytotoxic agents.

25 The present invention relates to methods of detecting a tumor that has p185 on tumor cell surfaces. The methods comprise the step of administering, to an individual suspected of having such a tumor or being susceptible to such a tumor, a conjugated composition that comprises such peptides linked
30 to detectable agents and detecting the presence of localized conjugated composition within the body of the individual.

The present invention relates to pharmaceutical compositions which comprise such peptides and/or conjugated compositions in combination with a pharmaceutically acceptable
35 carrier or diluent.

The present invention relates to methods of preventing transformation of a normal cell into a tumor cell in an

- 6 -

individual at risk of developing a tumor having tumor cells which have p185 on their surfaces. The method comprises the steps of: identifying such an individual; and administering to the individual such peptides.

- 5 The present invention relates to methods of treating an individual who has cancer characterized by tumor cells that have a p185 on their cell surfaces. The methods comprise the steps of: identifying such an individual; and administering to the individual, a therapeutically effective amount of such
- 5 peptides and/or conjugated compositions.

DETAILED DESCRIPTION OF THE INVENTION

As used herein, the terms "neu-associated cancer", "erbB-2-associated cancer", "neu-associated tumors", "erbB-2-associated tumors", "p185-mediated tumors" and "p185-associated

10 tumors" are meant to refer to tumor cells and neoplasms which express the *erbB-2* gene to produce p185. Examples of *erbB-2*-associated cancer include many human adenocarcinomas. Breast, ovary, lung, pancreas, salivary gland and kidney adenocarcinomas and prostate, and some neuroblastoma have been

15 found to be *erbB-2*-associated cancers.

When a therapeutically effective amount of a compound of the invention is administered to an individual who has *erbB-2*-associated cancer, the effect is that the proliferation rate of tumor cells is slowed down or eliminated. As used herein,

20 the term "compound" is meant to refer to a peptide or a peptide mimetic which is useful in the method of detecting, imaging, treating or preventing p185-mediated tumors.

As used herein, the term "therapeutically effective amount" is meant to refer to an amount of a compound which

25 produces a medicinal effect observed as reduction or reverse in tumorigenic phenotype of tumor cells in an individual when a therapeutically effective amount of a compound is administered to an individual who is susceptible to or

30 suffering from p185-mediated tumors. Therapeutically effective amounts are typically determined by the effect they have compared to the effect observed when a composition which

- 7 -

includes no active ingredient is administered to a similarly situated individual.

As used herein, the term "high risk individual" is meant to refer to an individual who has had a *erbB-2*-associated tumor either removed or enter remission and who is therefore susceptible to a relapse or recurrence. As part of a treatment regimen for a high risk individual, the individual can be prophylactically treated to conduct the recurrence of the *erbB-2*-associated tumors. Thus, once it is known that an individual has had cancer characterized by tumor cells with p185 on their cell surfaces, the individual can be treated according to the present invention to prevent normal cells from transforming into tumor cells.

As used herein, the term "preventing the development of tumors" is meant to refer to preventing the transformation of normal cells into tumor cells. Thus, the development of tumors refers to the transformation event which results in the loss of a normal phenotype and the acquisition of a transformed phenotype. According to some aspects of the present invention, compounds may be administered to individuals who are at risk of developing tumors. The prophylactic administration of compounds of the invention to high risk individuals results in the prevention of the transformation event occurring. Cells having the normal phenotype are not converted to the cells having transformed phenotype. The compounds of the invention prevent tumors before they are formed by preventing a normal cell from becoming a cancer cell.

As used herein, the term "prophylactically effective amount" is meant to refer to an amount of a compound which produces a medicinal effect observed as the prevention of non-transformed cells from becoming transformed in an individual when a prophylactically effective amount of a compound is administered to an individual who is susceptible to p185-mediated tumors. Prophylactically effective amounts are typically determined by the effect they have compared to the effect observed when a composition which includes no active ingredient is administered to a similarly situated individual.

- 8 -

As used herein, the terms "conformationally restricted peptides", "constrained peptides" and "conformationally constrained peptides" are used interchangeably and are meant to refer to peptides which, for example through intramolecular bonds, are conformationally stable and remain in a sufficiently restricted conformation. The compounds have an affinity to p185 and, when bound to p185 as cells, a biologically active effect on cells that have a p185-mediated transformation phenotype.

As used herein, the terms "aromatic amino acids" and "aromatic amino acid residues" used interchangeably are meant to refer to phenylalanine and tyrosine.

As used herein, the term "exocyclic amino acid residue" is meant to refer to amino acid residues which are linked to cyclicized peptide but which are not within the portion of the peptide that makes up the circularized structure.

As used herein, the term "exocyclic portions" is meant to refer to an amino acid sequence having one or more amino acid residues which is linked to cyclicized peptide but which are not within the portion of the peptide that makes up the circularized structure.

As used herein, the term "linking moiety" is meant to refer to a molecular component or functional group which is capable of forming bonds with three amino acids.

As used herein, the term "linking amino acid residue" is meant to refer to an amino acid residue that is a linking moiety.

As used herein, the terms "active sequence" and "active region" are used interchangeably and are meant to refer to the amino acid sequence of the portion of a compound of the invention that is directly interacts with p185, wherein the interaction is characterized by an affinity between the active portion and p185.

The present invention relates to constrained peptides that contain exocyclic portions including exocyclic amino acids that are aromatic amino acids as well as an active region which

- 9 -

specifically binds to p185. Co-pending U.S. Serial Number 08/257,783 filed June 10, 1994 and entitled "Constrained Peptides" is incorporated herein by reference in its entirety.

The present invention is useful to therapeutically
110 treat an individual identified as suffering from *erbB*-2-associated tumors in order to reverse the transformed phenotype of the tumor cells. The present invention is useful to prophylactically treat an individual who is predisposed to develop *erbB*-2-associated tumors or who has had *erbB*-2-
115 associated tumors and is therefore susceptible to a relapse or recurrence. The present invention is useful to detectably image tumors with respect to p185 on their surfaces. The present invention is useful to detect and quantify p185 on all surfaces.

The translation product of the *erbB*-2 oncogene is p185, a transmembrane glycoprotein having tyrosine kinase activity and a molecular weight of about 185,000 daltons as determined by carrying out electrophoresis on the glycoprotein and comparing its movement with marker proteins of known
125 molecular weight. Experiments have shown that p185 forms homodimers with other p185 molecules or heterodimers with epidermal growth factor receptor (EGFR) and that these dimers exhibit elevated tyrosine kinase activity which brings about the transformed phenotype in cells having such dimers. It is
130 believed that dimerization of p185 with other membrane bound receptors, such as other p185 molecules or EGFR, results in elevated levels of tyrosine kinase activity and the transformed phenotype.

According to the present invention, compounds bind to
135 p185 and thereby prevent the dimerization with other membrane bound receptors by down modulation of their surface receptors. When bound to p185, the compounds of the invention induce internalization of the receptor which results in elimination or reduction of tyrosine kinase activity. The elimination or
140 reduction of tyrosine kinase activity results in an elimination or reduction in cell proliferation levels and a non-transformed, quiescent phenotype. The compounds of the

- 10 -

invention cause down-modulation of *erbB-2* cell surface reception. When bound to p185, the compounds of the invention reverse the transformed state of such cells, resulting in decreasing the rate of transformation in cells showing intact non-activated tyrosine kinase receptors found in normal cells are not affected by the compounds of the invention and hence are non-toxic.

The compounds of the invention are therefore useful in the treatment of individuals suspected of having from p185-mediated tumors. When administered to individuals who have been thusly identified, the compounds of the invention bind to p185, thereby causing modulation of *erbB-2* receptors. The p185 receptor bound to the compound internalize and the internalization of the p185 receptor contributes to the decrease in tyrosine kinase activity of the p185 receptors. When the tyrosine kinase activity in the cell is reduced from the elevated levels associated with amplified or overexpressed p185, the cell becomes quiescent and displays a non-transformed phenotype.

The compounds of the invention are also useful in the prevention of p185-mediated tumor formation and therefore in the method of prophylactically treating high risk individuals from developing p185-mediated tumors. That is, the prophylactic administration of compounds of the invention results in the prevention of cells that over express p185 from becoming transformed. The cells in the individuals which would turn into tumors in an untreated individual never become transformed and never become tumors in individuals treated by the methods of the invention. When administered to individuals who have been identified as being susceptible to or otherwise at risk of developing tumors, the compounds of the invention bind to p185, thereby preventing and cause the internalization of the receptor/compound complex. The p185 receptor bound to the compound internalizes and the bound p185 receptor does not contribute the elevation in tyrosine kinase activity associated with dimerized p185 receptors. The tyrosine kinase activity

- 11 -

180 in the cell never become sufficiently elevated and the cell remains non-transformed.

The compounds of the invention can be labelled or otherwise made detectable. As a detectable compound that binds to p185, the compounds are useful as imaging agents and reagents in diagnostic procedures that are used to identify a tumor as being a p185-associated tumor. Labelled compounds of the invention can be administered to individuals suspected of suffering from p185-associated tumors. The labelled compounds will bind to the high density of p185 on cells and thereby accumulate on p185-associated tumor cells. Using standard imaging techniques, the site of the tumors can be detected.

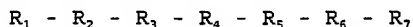
One aspect of the invention therefore relates to methods of imaging p185-associated tumors. Such methods comprise the steps of administering a detectable compound of the invention to an individuals who is suffering from or susceptible to erbB-2-associated cancer and detecting the location of the detectable compound within the body of the individual.

The compounds bind to p185 that is present on cell surfaces and are therefore useful as diagnostic/characterizing reagents in diagnostic kits. When a tissue sample from an individual is contacted with a compound of the invention, the compound will bind to the p185 present on cells. The level of p185 expression can be quantified. Labelled compounds of the invention are also useful as *in vitro* reagents to quantify the amount of p185 present in the cell. Such information indicates whether or not a tumor is p185 mediated and therefore, whether specific treatments should be used or avoided. Using standard techniques, samples believed to include tumor cells are obtained and contacted with labelled compounds of the active region of the invention. After removing any unbound labelled compounds, the quantity of labelled compound bound to the cell or the quantity of removed as unbound labelled compounds is determined. The information directly relates to the amount of p185 the cell expresses and thus can be used to determine whether a cell is over expressing p185. Overexpression of p185

- 12 -

indicates p185-mediated transformation. This information is useful in formulating the prognosis and course of treatment to be imposed on the individual. Kits of the invention comprise detectable compounds of the invention and instructions for performing assays of the invention. Optionally, kits may also contain one or more of the following: containers which comprise positive controls, containers which comprise negative controls, photographs of representative examples of positive results and photographs of representative examples of negative results.

According to some embodiments, the present invention provides peptides having the formula:



wherein:

R_1 is 1-6 amino acid residues and at least one of which is tyrosine or phenylalanine;

R_2 is a linking moiety which bonds with R_1 , R_3 and R_6 such that a portion of the molecule is cyclicized;

R_3 is 0-20 amino acids;

R_4 is 6 amino acids;

R_5 is 0-20 amino acids;

R_6 is a linking moiety which bonds with R_5 , R_7 and R_2 such that a portion of the molecule is cyclicized;

R_7 is 1-6 amino acid residues and at least one of which is tyrosine or phenylalanine;

wherein: R_1 , R_2 , R_3 , R_4 , R_5 , R_6 and R_7 , taken together, are 30 amino acids or less;

and R_4 is has the formula:



wherein:

either,

R_{41} is E or D;

R_{42} is N or Q;

R_{43} is W;

R_{44} is D or E;

R_{45} is W; and,

R_{46} is Y or F;

or

- 13 -

255 R₄₁ is G, V, A, I or L;
 R₄₂ is D or E;
 R₄₃ is G, V, A, I or L;
 R₄₄ is F or Y;
 R₄₅ is Y or F; and,
 R₄₆ is A, I, L, G or V; .

260 The primary function of R₁ in compounds of the present
invention arises from the presence of at least one amino acid
that contains an aromatic group: i.e. the presence of tyrosine
or phenylalanine. The presence of the aromatic amino acid at
position R₁ results in an increase affinity of the peptide to
p185 and an attendant increase in activity of the compound.
265 In embodiments where additional amino acid residues are
present, they can present the aromatic amino acid in a more
effective position to further increase the affinity and
activity of the compound. Additional amino acids that may be
present must not eliminate the effect that the aromatic amino
270 acid has on affinity or activity. Examples of amino acid
sequences which may be used as R₁ are disclosed in co-pending
U.S. Serial Number 08/257,783. In some embodiments, the
additional amino acids are present as a site for linkage to
detectable labels or moieties. In some embodiments, the
275 additional amino acids are present as a site for dimerization
with other peptides; either for formation of homodimers with
each other or heterodimers with other peptides. In some
preferred embodiments, R₁ is 1-5 amino acids. In some
preferred embodiments, R₁ is 4 amino acids. In some preferred
280 embodiments, R₁ is 3 amino acids. In some preferred
embodiments, R₁ is 2 amino acids. In some preferred
embodiments, R₁ is 1 amino acid. In some preferred
embodiments, R₁ comprises F-E. In some preferred embodiments,
R₁ consists of F-E. In some preferred embodiments, R₁
285 comprises of Y-E. In some preferred embodiments, R₁ consists
of Y-E. In some preferred embodiments, R₁ comprises F. In
some preferred embodiments, R₁ consists of F. In some
preferred embodiments, R₁ comprises Y. In some preferred
embodiments, R₁ consists of Y. Other examples of R₁ include F-

- 14 -

290 K-T-N-K (SEQ ID NO:1) and F-G-Q. Contemplated equivalents include aromatic functional groups at R₁ which are not part of tyrosine or phenylalanine.

The function of R₂ is to form bonds with R₁ as well as to form bonds with R₆ which cyclicize or otherwise
295 conformationally restrict the molecule. Bonds between R₂ and R₆ cyclicize the molecule and thereby maintain R₃-R₄-R₅, and, specifically R₄, in a constrained conformation which produces the specific biologically active surface that has an affinity for and interacts with p185. Further, in such an arrangement
300 R₁ becomes an exocyclic portion of the peptide. Accordingly, R₂ may be any moiety capable of forming bonds with R₆ as well as R₁ and R₃. R₂ is preferably an amino acid residue, most preferably cysteine. When both R₂ and R₆ are cysteine, the disulfide bonds form between the two cysteines cyclicize the
305 molecule. It is contemplated that R₂ may any moiety that, together with R₆, will allow for the cyclization of the portion of the molecule that includes R₁-R₂-R₃-R₄-R₅-R₆ while rendering R₁ and R₇ exocyclic portions of the peptide. Those having ordinary skill in the art can readily prepare peptides
310 according to the present invention in which R₂ and R₆ are moieties capable of forming bonds to each other. The cyclization of linear peptides using disulfide bonds between non-adjacent cysteines is well known. Similarly, other non-adjacent amino acid residues may be linked to cyclicize a
315 peptide sequence and the means to do so are similarly well known. Other methods of cyclization include those described by Di Blasio, et al., (1993) *Biopolymers*, 33:1037-1049; Wood, et al., (1992) *J. Pep. Prot. Res.*, 39:533-539; Saragovi, et al., (1992) *Immunomethods*, 1:5-9; Saragovi, et al., (1991)
320 *Science*, 253:792-795; Manning, et al., (1993) *Reg. Peptides*, 45:279-283; Hruby, (1993) *Biopolymers*, 33:1073-1082; Bach, et al., (1994) *New Adv. Peptidomimetics Small Mol. Design*, 1:1-26; and Matsuyama, et al., (1992) *J. Bacteriol.*, 174:1769-1776, each of which are incorporated herein by reference.

325 The function of R₃ is to serve as spacers and provide structure to present the active region in proper conformation.

- 15 -

In some embodiments, the cyclization of the active region by particular linking moieties results in the proper folding of the active region to place it in active conformation and no R₃ is required. In some embodiments, the cyclization of the active region by particular linking moieties requires additional spacing and turns to facilitate that proper folding of the active region in order to place it in active conformation. In such embodiments, amino acid residues or sequences may be provided at R₃. In some preferred embodiments, R₃ is 0-10 amino acids. In some preferred embodiments, R₃ is 0-5 amino acids. In some preferred embodiments, R₃ is 0 amino acids.

R₄ is the active region of the compounds according to this aspect of the invention. In compounds of the invention, the functional groups of the active region are in a conformation which places them in a particular three dimensional arrangement that allows them to interact with the amino acids and functional groups thereon of p185 and to bind to p185 through such interactions. In peptide mimetics, the functional groups are provided in the active three dimensional arrangement but are connected to modified or different backbones.

In some preferred embodiments, R₄ is E-N-W-D-W-Y (SEQ ID NO:2), D-N-W-D-W-Y (SEQ ID NO:3), E-Q-W-D-W-Y (SEQ ID NO:4), D-Q-W-D-W-Y (SEQ ID NO:5), E-N-W-E-W-Y (SEQ ID NO:6), D-N-W-E-W-Y (SEQ ID NO:7), E-Q-W-E-W-Y (SEQ ID NO:8), D-Q-W-E-W-Y (SEQ ID NO:9), E-N-W-D-W-F (SEQ ID NO:10), D-N-W-D-W-F (SEQ ID NO:11), E-Q-W-D-W-F (SEQ ID NO:12), D-Q-W-D-W-F (SEQ ID NO:13), E-N-W-E-W-F (SEQ ID NO:14), D-N-W-E-W-F (SEQ ID NO:15), E-Q-W-E-W-F (SEQ ID NO:16) or D-Q-W-E-W-F (SEQ ID NO:17). In some preferred embodiments, R₄ is E-N-W-D-W-Y (SEQ ID NO:2).

In some preferred embodiments, R₄ is G/V/A/I/L-D/E-G/V/A/I/L-F/Y-Y/F-A/G/V/I/L (SEQ ID NO:18). It is possible to vary each residue with one that contributes equivalent bulk and hydrophobic moment and that still permits hydrogen bonding to surrounding water molecules or to residues to which the compound attaches. SEQ ID NO:18 represents a formula for

- 16 -

defining each of the permutations of possible variations in sequence within the scope of the invention. In some preferred
365 embodiments, R_4 is G-D-G-F-Y-A (SEQ ID NO:19), G-E-G-F-Y-A (SEQ ID NO:20), G-D-G-Y-Y-A (SEQ ID NO:21), G-E-G-Y-Y-A (SEQ ID NO:22), G-D-G-F-F-A (SEQ ID NO:23), G-E-G-F-F-A (SEQ ID NO:24), G-D-G-Y-F-A (SEQ ID NO:25), G-E-G-Y-F-A (SEQ ID NO:26), A-D-G-F-Y-A (SEQ ID NO:27), A-E-G-F-Y-A (SEQ ID NO:28), A-D-G-Y-Y-A (SEQ ID NO:29), A-E-G-Y-Y-A (SEQ ID NO:30), A-D-G-F-F-A (SEQ ID NO:31), A-E-G-F-F-A (SEQ ID NO:32), A-D-G-Y-F-A (SEQ ID NO:33), A-E-G-Y-F-A (SEQ ID NO:34), G-D-A-F-Y-A (SEQ ID NO:35), G-E-A-F-Y-A (SEQ ID NO:36), G-D-A-Y-Y-A (SEQ ID NO:37), G-E-A-Y-Y-A (SEQ ID NO:38), G-D-A-F-F-A (SEQ ID NO:39), G-E-A-F-F-A (SEQ ID NO:40), G-D-A-Y-F-A (SEQ ID NO:41), G-E-A-Y-F-A (SEQ ID NO:42), A-D-A-F-Y-A (SEQ ID NO:43), A-E-A-F-Y-A (SEQ ID NO:44), A-D-A-Y-Y-A (SEQ ID NO:45), A-E-A-Y-Y-A (SEQ ID NO:46), A-D-A-F-F-A (SEQ ID NO:47), A-E-A-F-F-A (SEQ ID NO:48), A-D-A-Y-F-A (SEQ ID NO:49), A-E-A-Y-F-A (SEQ ID NO:50), G-D-G-F-Y-G (SEQ ID NO:51), G-E-G-F-Y-G (SEQ ID NO:52), G-D-G-Y-Y-G (SEQ ID NO:53), G-E-G-Y-Y-G (SEQ ID NO:54), G-D-G-F-F-G (SEQ ID NO:55), G-E-G-F-F-G (SEQ ID NO:56), G-D-G-Y-F-G (SEQ ID NO:57), G-E-G-Y-F-G (SEQ ID NO:58), A-D-G-F-Y-G (SEQ ID NO:59), A-E-G-F-Y-G (SEQ ID NO:60), A-D-G-Y-Y-G (SEQ ID NO:61), A-E-G-Y-Y-G (SEQ ID NO:62), A-D-G-F-F-G (SEQ ID NO:63), A-E-G-F-F-G (SEQ ID NO:64), A-D-G-Y-F-G (SEQ ID NO:65), A-E-G-Y-F-G (SEQ ID NO:66), G-D-A-F-Y-G (SEQ ID NO:67), G-E-A-F-Y-G (SEQ ID NO:68), G-D-A-Y-Y-G (SEQ ID NO:69), G-E-A-Y-Y-G (SEQ ID NO:70), G-D-A-F-F-G (SEQ ID NO:71), G-E-A-F-F-G (SEQ ID NO:72), G-D-A-Y-F-G (SEQ ID NO:73), G-E-A-Y-F-G (SEQ ID NO:74), A-D-A-F-Y-G (SEQ ID NO:75), A-E-A-F-Y-G (SEQ ID NO:76), A-D-A-Y-Y-G (SEQ ID NO:77), A-E-A-Y-Y-G (SEQ ID NO:78), A-D-A-F-F-G (SEQ ID NO:79), A-E-A-F-F-G (SEQ ID NO:80), A-D-A-Y-F-G (SEQ ID NO:81), or A-E-A-Y-F-G (SEQ ID NO:82).
395

The function of R_5 is to present the active region in proper conformation. In some embodiments, the cyclization of the active region by particular linking moieties results in the proper folding of the active region to place it in active
400 conformation and no R_5 is required. In some embodiments, the

- 17 -

cyclization of the active region by particular linking moieties requires additional spacing and turns to facilitate that proper folding of the active region in order to place it in active conformation. In such embodiments, amino acid residues or
405 sequences may be provided at R_5 . In some preferred embodiments, R_5 is 0-10 amino acids. In some preferred embodiments, R_5 is 0-5 amino acids. In some preferred embodiments, R_5 is 0 amino acids.

The function of R_6 is to form bonds with R_2 which
410 cyclicize or otherwise conformationally restrict the molecule. Bonds between R_6 and R_2 cyclicize the molecule and thereby maintain R_3 - R_4 - R_5 , and, specifically R_4 , in a constrained conformation which produces the specific biologically active surface that has an affinity for and interacts with p185.
415 Accordingly, R_6 may be any moiety capable of forming bonds with R_2 as well as R_5 and R_7 . R_6 is preferably an amino acid residue, most preferably cysteine. When both R_6 and R_2 are cysteine, disulfide bonds formed between the two cysteines cyclicizes the molecule. It is contemplated that R_6 may any
420 moiety that, together with R_2 , will allow for the cyclization of the molecule. Those having ordinary skill in the art can readily prepare peptides according to the present invention in which R_2 and R_6 are moieties capable of forming bonds to each other. The cyclization of linear peptides using disulfide
425 bonds between non-adjacent cysteines is well known. Similarly, other non-adjacent amino acid residues may be linked to cyclicize a peptide sequence and the means to do so are similarly well known. Other methods of cyclization include those described by Di Blasio, et al., (1993) *Biopolymers*,
430 33:1037-1049; Wood, et al., (1992) *J. Pep. Prot. Res.*, 39:533-539; Saragovi, et al., (1992) *Immunomethods*, 1:5-9; Saragovi, et al., (1991) *Science*, 253:792-795; Manning, et al., (1993) *Reg. Peptides*, 45:279-283; Hruby, (1993) *Biopolymers*, 33:1073-1082; Bach, et al., (1994) *New Adv. Peptidomimetics Small Mol.*
435 *Design*, 1:1-26; and Matsuyama, et al., (1992) *J. Bacteriol.*, 174:1769-1776, each of which are incorporated herein by reference.

- 18 -

The primary function of R₁ in compounds of the present invention arises from the presence of at least one amino acid that contains an aromatic group: i.e. the presence of tyrosine or phenylalanine. The presence of the aromatic amino acid at position R₁ results in an increase affinity of the peptide to p185 and an attendant increase in activity of the compound. In embodiments where additional amino acid residues are present, they can present the aromatic amino acid in a more effective position to further increase the affinity and activity of the compound. Additional amino acids that may be present must not eliminate the effect that the aromatic amino acid has on affinity or activity. Examples of amino acid sequences which may be used as R₁ are disclosed in co-pending U.S. Serial Number 08/257,783. In some embodiments, the additional amino acids are present as a site for linkage to detectable labels or moieties. In some embodiments, the additional amino acids are present as a site for dimerization with other peptides; either for formation of homodimers with each other or heterodimers with other peptides. In some preferred embodiments, R₁ is 1-5 amino acids. In some preferred embodiments, R₁ is 4 amino acids. In some preferred embodiments, R₁ is 3 amino acids. In some preferred embodiments, R₁ is 2 amino acids. In some preferred embodiments, R₁ is 1 amino acid. In some preferred embodiments, R₁ comprises Y-P-P-G-C (SEQ ID NO:83). In some preferred embodiments, R₁ consists of Y-P-P-G-C (SEQ ID NO:83). In some preferred embodiments, R₁ comprises Y-M-D-V (SEQ ID NO:84). In some preferred embodiments, R₁ consists of Y-M-D-V (SEQ ID NO:84). In some preferred embodiments, R₁ comprises F. In some preferred embodiments, R₁ consists of F. In some preferred embodiments, R₁ comprises F-D-V. In some preferred embodiments, R₁ consists of F-D-V. In some preferred embodiments, R₁ comprises Y. In some preferred embodiments, R₁ consists of Y. Another example of R₁ is Q-F. Contemplated equivalents include aromatic functional groups at R₁ which are not part of tyrosine or phenylalanine.

- 19 -

In some preferred embodiments, R_1 and R_7 collectively
475 contain both tyrosine and phenylalanine. That is, if R_1
comprises tyrosine then R_7 comprises phenylalanine and if R_1
comprises phenylalanine then R_7 comprises tyrosine. In some
preferred embodiments, R_1 and R_7 do not both contain tyrosine
or phenylalanine. That is, if R_1 comprises tyrosine and not
480 phenylalanine then R_7 comprises phenylalanine and not tyrosine
and if R_1 comprises phenylalanine and not tyrosine then R_7
comprises tyrosine and not phenylalanine.

In some preferred embodiments, $R_1, R_2, R_3, R_4, R_5, R_6$
and R_7 , taken together, are less than 30 amino acids. In some
485 preferred embodiments, $R_1, R_2, R_3, R_4, R_5, R_6$ and R_7 , taken
together, are 20 amino acids or less. In some preferred
embodiments, $R_1, R_2, R_3, R_4, R_5, R_6$ and R_7 , taken together, are
less than 20 amino acids. In some preferred embodiments, $R_1,$
 R_2, R_3, R_4, R_5, R_6 and R_7 , taken together, are 15 amino acids.
490 In some preferred embodiments, $R_1, R_2, R_3, R_4, R_5, R_6$ and R_7 ,
taken together, are less than 15 amino acids. In some
preferred embodiments, $R_1, R_2, R_3, R_4, R_5, R_6$ and R_7 , taken
together, are 14 amino acids. In some preferred embodiments,
 $R_1, R_2, R_3, R_4, R_5, R_6$ and R_7 , taken together, are 13 amino
495 acids. In some preferred embodiments, $R_1, R_2, R_3, R_4, R_5, R_6$ and
 R_7 , taken together, are 12 amino acids. In some preferred
embodiments, $R_1, R_2, R_3, R_4, R_5, R_6$ and R_7 , taken together, are
11 amino acids. In some preferred embodiments, $R_1, R_2, R_3, R_4,$
 R_5, R_6 and R_7 , taken together, are 10 amino acids.

500 In some embodiments, the peptide is selected from the
group consisting of: F-E-C-E-N-W-D-W-Y-C-Y-P-P-G-C (SEQ ID
NO:85); F-C-G-D-G-F-Y-A-C-M-D-V (SEQ ID NO:86); F-E-C-D-N-W-D-
W-Y-C-Y-P-P-G-C (SEQ ID NO:87); F-E-C-E-Q-W-D-W-Y-C-Y-P-P-G-C
(SEQ ID NO:88); F-E-C-D-Q-W-D-W-Y-C-Y-P-P-G-C (SEQ ID NO:89);
505 F-E-C-E-N-W-E-W-Y-C-Y-P-P-G-C (SEQ ID NO:90); F-E-C-D-N-W-E-W-
Y-C-Y-P-P-G-C (SEQ ID NO:91); F-E-C-E-Q-W-E-W-Y-C-Y-P-P-G-C
(SEQ ID NO:92); F-E-C-D-Q-W-E-W-Y-C-Y-P-P-G-C (SEQ ID NO:93);
F-E-C-E-N-W-D-W-F-C-Y-P-P-G-C (SEQ ID NO:94); F-E-C-D-N-W-D-W-
F-C-Y-P-P-G-C (SEQ ID NO:95); F-E-C-E-Q-W-D-W-F-C-Y-P-P-G-C
510 (SEQ ID NO:96); F-E-C-D-Q-W-D-W-F-C-Y-P-P-G-C (SEQ ID NO:97);

- 21 -

NO:153); F-E-C-D-N-W-E-W-Y-C-Y-P-P-G-C (SEQ ID NO:154); F-E-C-E-Q-W-E-W-Y-C-Y-P-P-G-C (SEQ ID NO:155); F-E-C-D-Q-W-E-W-Y-C-Y-P-P-G-C (SEQ ID NO:156); F-E-C-E-N-W-D-W-F-C-Y-P-P-G-C (SEQ ID NO:157); F-E-C-D-N-W-D-W-F-C-Y-P-P-G-C (SEQ ID NO:158); F-E-C-E-Q-W-D-W-F-C-Y-P-P-G-C (SEQ ID NO:159); F-E-C-D-Q-W-D-W-F-C-Y-P-P-G-C (SEQ ID NO:160); F-E-C-E-N-W-E-W-F-C-Y-P-P-G-C (SEQ ID NO:161); F-E-C-D-N-W-E-W-F-C-Y-P-P-G-C (SEQ ID NO:162); F-E-C-E-Q-W-E-W-F-C-Y-P-P-G-C (SEQ ID NO:163); F-E-C-D-Q-W-E-W-F-C-Y-P-P-G-C (SEQ ID NO:164); F-C-E-N-W-D-W-Y-C-Y-P-P-G-C (SEQ ID NO:165); F-C-D-N-W-D-W-Y-C-Y-P-P-G-C (SEQ ID NO:166); F-C-E-Q-W-D-W-Y-C-Y-P-P-G-C (SEQ ID NO:167); F-C-D-Q-W-D-W-Y-C-Y-P-P-G-C (SEQ ID NO:168); F-C-E-N-W-E-W-Y-C-Y-P-P-G-C (SEQ ID NO:169); F-C-D-N-W-E-W-Y-C-Y-P-P-G-C (SEQ ID NO:170); F-C-E-Q-W-E-W-Y-C-Y-P-P-G-C (SEQ ID NO:171); F-C-D-Q-W-E-W-Y-C-Y-P-P-G-C (SEQ ID NO:172); F-C-E-N-W-D-W-F-C-Y-P-P-G-C (SEQ ID NO:173); F-C-D-N-W-D-W-F-C-Y-P-P-G-C (SEQ ID NO:174); F-C-E-Q-W-D-W-F-C-Y-P-P-G-C (SEQ ID NO:175); F-C-D-Q-W-D-W-F-C-Y-P-P-G-C (SEQ ID NO:176); F-C-E-N-W-E-W-F-C-Y-P-P-G-C (SEQ ID NO:177); F-C-D-N-W-E-W-F-C-Y-P-P-G-C (SEQ ID NO:178); F-C-E-Q-W-E-W-F-C-Y-P-P-G-C (SEQ ID NO:179); and F-C-D-Q-W-E-W-F-C-Y-P-P-G-C (SEQ ID NO:180).

In some embodiments, compounds of the invention have the formula:

570 $R_1 - R_2 - R_3 - R_4 - R_5 - R_6 - R_7$

wherein:

$R_1 - R_2 - R_3$ is F-C, Y-C, F-E-C, or Y-E-C;

R_4 is G/V/A/I/L-D/E-G/V/A/I/L-F/Y-Y/F-A/G/V/I/L (SEQ ID NO:18); and

575 $R_5 - R_6 - R_7$ is C-Y-P-P-G-C (SEQ ID NO:181), C-Y-M-D-V (SEQ ID NO:182), C-F, C-F-D-V (SEQ ID NO:183) or C-Y.

In some embodiments, compounds of the invention have the formula:

580 $R_1 - R_2 - R_3 - R_4 - R_5 - R_6 - R_7$

wherein:

$R_1 - R_2 - R_3$ is F-C, Y-C, F-E-C, or Y-E-C;

R_4 is G-D-G-F-Y-A (SEQ ID NO:19), G-E-G-F-Y-A (SEQ ID NO:20), G-D-G-Y-Y-A (SEQ ID NO:21), G-E-G-Y-Y-A (SEQ ID NO:22), G-D-G-F-F-A (SEQ ID NO:23), G-E-G-F-F-A (SEQ ID

- 22 -

585 NO:24), G-D-G-Y-F-A (SEQ ID NO:25), G-E-G-Y-F-A (SEQ ID NO:26),
A-D-G-F-Y-A (SEQ ID NO:27), A-E-G-F-Y-A (SEQ ID NO:28), A-D-G-
Y-Y-A (SEQ ID NO:29), A-E-G-Y-Y-A (SEQ ID NO:30), A-D-G-F-F-A
(SEQ ID NO:31), A-E-G-F-F-A (SEQ ID NO:32), A-D-G-Y-F-A (SEQ
ID NO:33), A-E-G-Y-F-A (SEQ ID NO:34), G-D-A-F-Y-A (SEQ ID
590 NO:35), G-E-A-F-Y-A (SEQ ID NO:36), G-D-A-Y-Y-A (SEQ ID NO:37),
G-E-A-Y-Y-A (SEQ ID NO:38), G-D-A-F-F-A (SEQ ID NO:39), G-E-A-
F-F-A (SEQ ID NO:40), G-D-A-Y-F-A (SEQ ID NO:41), G-E-A-Y-F-A
(SEQ ID NO:42), A-D-A-F-Y-A (SEQ ID NO:43), A-E-A-F-Y-A (SEQ
ID NO:44), A-D-A-Y-Y-A (SEQ ID NO:45), A-E-A-Y-Y-A (SEQ ID
595 NO:46), A-D-A-F-F-A (SEQ ID NO:47), A-E-A-F-F-A (SEQ ID NO:48),
A-D-A-Y-F-A (SEQ ID NO:49), A-E-A-Y-F-A (SEQ ID NO:50), G-D-G-
F-Y-G (SEQ ID NO:51), G-E-G-F-Y-G (SEQ ID NO:52), G-D-G-Y-Y-G
(SEQ ID NO:53), G-E-G-Y-Y-G (SEQ ID NO:54), G-D-G-F-F-G (SEQ
ID NO:55), G-E-G-F-F-G (SEQ ID NO:56), G-D-G-Y-F-G (SEQ ID
600 NO:57), G-E-G-Y-F-G (SEQ ID NO:58), A-D-G-F-Y-G (SEQ ID NO:59),
A-E-G-F-Y-G (SEQ ID NO:60), A-D-G-Y-Y-G (SEQ ID NO:61), A-E-G-
Y-Y-G (SEQ ID NO:62), A-D-G-F-F-G (SEQ ID NO:63), A-E-G-F-F-G
(SEQ ID NO:64), A-D-G-Y-F-G (SEQ ID NO:65), A-E-G-Y-F-G (SEQ
ID NO:66), G-D-A-F-Y-G (SEQ ID NO:67), G-E-A-F-Y-G (SEQ ID
605 NO:68), G-D-A-Y-Y-G (SEQ ID NO:69), G-E-A-Y-Y-G (SEQ ID NO:70),
G-D-A-F-F-G (SEQ ID NO:71), G-E-A-F-F-G (SEQ ID NO:72), G-D-A-
Y-F-G (SEQ ID NO:73), G-E-A-Y-F-G (SEQ ID NO:74), A-D-A-F-Y-G
(SEQ ID NO:75), A-E-A-F-Y-G (SEQ ID NO:76), A-D-A-Y-Y-G (SEQ
ID NO:77), A-E-A-Y-Y-G (SEQ ID NO:78), A-D-A-F-F-G (SEQ ID
610 NO:79), A-E-A-F-F-G (SEQ ID NO:80), A-D-A-Y-F-G (SEQ ID NO:81),
or A-E-A-Y-F-G (SEQ ID NO:82); and

R_5 - R_6 - R_7 is C-Y-P-P-G-C (SEQ ID NO:181), C-Y-M-
D-V (SEQ ID NO:182), C-F, C-F-D-V (SEQ ID NO:183) or C-Y.

Some examples of compounds of the invention include
615 compounds 1-1280.

In compounds 1-64:

R_1 - R_2 - R_3 is F-C,

R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and

R_5 - R_6 - R_7 is C-Y-P-P-G-C (SEQ ID NO:181).

620 In compounds 65-128:

R_1 - R_2 - R_3 is F-C,

- 23 -

R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 R_5 - R_6 - R_7 is C-Y-M-D-V (SEQ ID NO:182).

In compounds 129-192:

625

R_1 - R_2 - R_3 is F-C,

R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 R_5 - R_6 - R_7 is C-F.

In compounds 193-256:

R_1 - R_2 - R_3 is F-C,

630

R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 R_5 - R_6 - R_7 is C-F-D-V (SEQ ID NO:183).

In compounds 257-320:

R_1 - R_2 - R_3 is F-C,

635

R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 R_5 - R_6 - R_7 is C-Y.

In compounds 321-384:

R_1 - R_2 - R_3 is Y-C,

R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 R_5 - R_6 - R_7 is C-Y-P-P-G-C (SEQ ID NO:181).

640

In compounds 385-448:

R_1 - R_2 - R_3 is Y-C,

R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 R_5 - R_6 - R_7 is C-Y-M-D-V (SEQ ID NO:182).

In compounds 449-512:

645

R_1 - R_2 - R_3 is Y-C,

R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 R_5 - R_6 - R_7 is Y-F.

In compounds 513-576:

R_1 - R_2 - R_3 is Y-C,

650

R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 R_5 - R_6 - R_7 is C-F-D-V (SEQ ID NO:183).

In compounds 577-640:

R_1 - R_2 - R_3 is Y-C,

R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 R_5 - R_6 - R_7 is C-Y.

655

In compounds 641-704:

R_1 - R_2 - R_3 is F-E-C,

R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and

- 24 -

- 660 $R_5-R_6-R_7$ is C-Y-P-P-G-C (SEQ ID NO:181).
In compounds 705-768:
 $R_1-R_2-R_3$ is F-E-C,
 R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 $R_5-R_6-R_7$ is C-Y-M-D-V (SEQ ID NO:182).
In compounds 769-832:
665 $R_1-R_2-R_3$ is F-E-C,
 R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 $R_5-R_6-R_7$ is Y-F.
In compounds 833-896:
 $R_1-R_2-R_3$ is F-E-C,
670 R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 $R_5-R_6-R_7$ is C-F-D-V (SEQ ID NO:183).
In compounds 897-960:
 $R_1-R_2-R_3$ is F-E-C,
 R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
675 $R_5-R_6-R_7$ is C-Y.
In compounds 961-1024:
 $R_1-R_2-R_3$ is Y-E-C,
 R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 $R_5-R_6-R_7$ is C-Y-P-P-G-C (SEQ ID NO:181).
680 In compounds 1025-1088:
 $R_1-R_2-R_3$ is Y-E-C,
 R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 $R_5-R_6-R_7$ is C-Y-M-D-V (SEQ ID NO:182).
In compounds 1089-1152:
685 $R_1-R_2-R_3$ is Y-E-C,
 R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 $R_5-R_6-R_7$ is Y-F.
In compounds 1153-1216:
 $R_1-R_2-R_3$ is Y-E-C,
690 R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
 $R_5-R_6-R_7$ is C-F-D-V (SEQ ID NO:183).
In compounds 1217-1280:
 $R_1-R_2-R_3$ is Y-E-C,
 R_4 is one of SEQ ID NO:19 - SEQ ID NO:82, and
695 $R_5-R_6-R_7$ is C-Y.

- 25 -

In some preferred embodiment the compound is F-C-G-D-G-F-Y-A-C-Y-M-D-V (SEQ ID NO:184).

Those having ordinary skill in the art can readily construct molecules according to the above formulae and determine whether or not the compounds are active as p185 binding compounds which prevent and eliminate the p185-mediated transformation phenotype.

The peptides of the invention may be dimerized with each other to form homodimers or with other compounds including compounds of the invention to form heterodimers. In preferred dimers, the residues involved in the chemical bound which links the monomers is in the R₁ position of the compounds of the invention.

The compositions used in the method of treating, preventing or imaging tumors or quantifying p185 may comprise mimetics instead of peptides. As used herein, the term "Mimetics" is used to refer to compounds which mimic the activity of peptide. Mimetics are non-peptides but may comprise amino acids linked by non-peptide bonds. Parent application U.S. application serial number 07/940,654 filed September 3, 1992 and parent applications thereof, all of which are incorporated herein by reference, contain detailed guidance on the production of mimetics. Briefly, the three dimensional structure of the peptides which specifically interacts with the three dimensional structure of the p185 is duplicated by a molecule that is not a peptide.

The compounds of the invention may be used to treat individuals suffering from p185-associated tumors. According to one aspect of the invention, compounds are administered to individuals suspected of having p185 tumors. Those having ordinary skill in the art can readily determine whether an individual may have a tumor likely to be a p185 associated tumor. Biopsy protocols can be performed to identify tumor samples and determine whether or not they are p185 associated tumors. The diagnostic/characterization protocol described above may be used in the characterization and determination of p185 levels present on cell samples.

- 26 -

The compounds of the invention may be used to prevent the occurrence of p185 associated tumors in individuals susceptible to p185-associated tumors. According to one aspect of the invention, compounds are administered prophylactically to individuals susceptible to developing p185 tumors. Those having ordinary skill in the art can readily determine whether an individual may be susceptible to p185 associated tumors. The invention is particularly useful in high risk individuals who, for example, have a family history of erbB-2-associated cancer or show a genetic predisposition. Additionally, the present invention is particularly useful to prevent patients who have had erbB-2-associated tumors removed by surgical resection or who have been diagnosed as having erbB-2-associated cancer in remission.

Methods of the present invention comprise administering a single or multiple doses of the compounds of the invention. Preferred for human pharmaceutical use are pharmaceutical compositions that comprise the compounds of the present invention in combination with a pharmaceutically acceptable carrier or diluent.

The pharmaceutical compositions of the present invention may be administered by any means that enables the active agent to reach the agent's site of action in the body of a mammal. In the case of the peptides of the invention, the primary focus is the ability to reach and bind with cellular p185. Because proteins are subject to being digested when administered orally, parenteral administration, i.e., intravenous, subcutaneous, intramuscular, would ordinarily be used to optimize absorption. These small compact forms are resistant to many proteases and should be orally available.

In addition to pharmaceutical compositions which comprise compounds of the invention alone or in combination with other cancer therapeutics, therapeutic and diagnostic pharmaceutical compositions of the present invention include conjugated compounds specifically targeted to p185. The pharmaceutical compositions which comprise conjugated

- 27 -

770 compositions of the present invention may be used to diagnose or treat individuals suffering from p185-associated cancer.

One aspect of the present invention relies upon the use of a compound of the invention conjugated to a detectable and/or cytotoxic agent. In conjugated compositions, the compound of the invention delivers the active agent to cells
775 that have p185. Thus, cells which overexpress p185 will be contacted with more active agents than other cells. The active agent is useful to image, inhibit proliferation of and/or kill the cell. According to one aspect of the present invention, the active agent is a therapeutic agent or an imaging agent.

780 Some chemotherapeutic agents may be used as active agents and conjugated with compounds of the invention. Chemotherapeutics are typically, small chemical entities produced by chemical synthesis and include cytotoxic drugs, cytostatic drugs as well as compounds which affects cells in
785 other ways such as reversal of the transformed state to a differentiated state or those which inhibit cell replication. Examples of chemotherapeutics include, but are not limited to: methotrexate (amethopterin), doxorubicin (adrimycin), daunorubicin, cytosinarabioside, etoposide, 5-4 fluorouracil,
790 melphalan, chlorambucil, and other nitrogen mustards (e.g. cyclophosphamide), cis-platinum, vindesine (and other vinca alkaloids), mitomycin and bleomycin.

Active agents may be toxins: complex toxic products of various organisms including bacteria, plants, etc.
795 Examples of toxins include but are not limited to: ricin, ricin A chain (ricin toxin), *Pseudomonas* exotoxin (PE), diphtheria toxin (DT), *Clostridium perfringens* phospholipase C (PLC), bovine pancreatic ribonuclease (BPR), pokeweed antiviral protein (PAP), abrin, abrin A chain (abrin toxin), cobra venom factor (CVF), gelonin (GEL), saporin (SAP), modeccin, viscumin and volkensin. Protein toxins may be produced using
800 recombinant DNA techniques as fusion proteins which include peptides of the invention. Protein toxins may also be conjugated to compounds of the invention by non-peptidyl bonds.

- 28 -

805 Radioisotopes may be conjugated to compounds of the
invention to provide compositions that are useful as
therapeutic agents or for imaging procedures. Examples of
radioisotopes which useful in radiation therapy include: ^{47}Sc ,
 ^{67}Cu , ^{90}Y , ^{109}Pd , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{199}Au , ^{211}At , ^{212}Pb and
810 ^{212}Bi . Example of radioisotopes useful in imaging procedures
include: ^{43}K , ^{52}Fe , ^{57}Co , ^{67}Cu , ^{67}Ga , ^{68}Ga , ^{77}Br , $^{81}\text{Rb}/^{81\text{M}}\text{Kr}$, $^{87\text{M}}\text{Sr}$,
 $^{99\text{M}}\text{Tc}$, ^{111}In , $^{113\text{M}}\text{In}$, ^{123}I , ^{125}I , ^{127}Cs , ^{129}Cs , ^{131}I , ^{132}I , ^{197}Hg , ^{203}Pb and
 ^{206}Bi .

Imaging agents are useful in diagnostic procedures as
815 well as the procedures used to identify the location of p185
associated tumors. Imaging can be performed by many procedures
well-known to those having ordinary skill in the art and the
appropriate imaging agent useful in such procedures may be
conjugated to compounds of the invention by well-known means.
820 Imaging can be performed, for example, by radioscintigraphy,
nuclear magnetic resonance imaging (MRI) or computed tomography
(CT scan). The most commonly employed radiolabels for imaging
agents include radioactive iodine and indium. Imaging by CT
scan may employ a heavy metal such as iron chelates. MRI
825 scanning may employ chelates of gadolinium or manganese.
Additionally, positron emission tomography (PET) may be
possible using positron emitters of oxygen, nitrogen, iron,
carbon, or gallium.

Radiolabels are conjugated to compounds of the
830 invention by a variety of well-known techniques readily
performed without undue experimentation by those having
ordinary skill in the art. Radiolabels retain their
radioactivity irrespective of conjugation. Conjugation may be
accomplished directly between the compound and the radioisotope
835 or linking, intermediate molecular groups may be provided
between the compound and the radioisotope. Crosslinkers are
particularly useful to facilitate conjugation by providing
attachment sites for each moiety. Crosslinkers may include
additional molecular groups which serve as spacers to separate
840 the moieties from each other to prevent either from interfering
with the activity of the other. Often imaging can be imaged

- 29 -

using fluorescein , which are activated by light. (e.g. fluorescein (green), phycoerythrin (orange), P-E-cyanine-5 (red), P-E-texas red (red), cyanine-3 (orange), cyananine-5
845 (red), AMCA (ultraviolet detection))

One having ordinary skill in the art may conjugate a compound of the invention to a chemotherapeutic drug using well-known techniques. For example, Magerstadt, M. *Antibody Conjugates and Malignant Disease*. (1991) CRC Press, Boca Raton,
850 USA, pp. 110-152) which is incorporated herein by reference, teaches the conjugation of various cytostatic drugs to amino acids of antibodies. Such reactions may be applied to conjugate chemotherapeutic drugs to the compounds of the invention. Compounds of the invention such as peptides which
855 have a free amino group may be conjugated to active agents at that group. Most of the chemotherapeutic agents currently in use in treating cancer possess functional groups that are amenable to chemical crosslinking directly with proteins. For example, free amino groups are available on methotrexate,
860 doxorubicin, daunorubicin, cytosinarabioside, cis-platin, vindesine, mitomycin and bleomycin while free carboxylic acid groups are available on methotrexate, melphalan, and chlorambucil. These functional groups, that is free amino and carboxylic acids, are targets for a variety of homobifunctional
865 and heterobifunctional chemical crosslinking agents which can crosslink these drugs directly to the single free amino group of a compound of the invention.

Pharmaceutical compositions of the present invention may be administered either as individual therapeutic agents or
870 in combination with other therapeutic agents. They can be administered alone, but are generally administered with a pharmaceutical carrier selected on the basis of the chosen route of administration and standard pharmaceutical practice.

The dosage administered will, of course, vary
875 depending upon known factors such as the pharmacodynamic characteristics of the particular agent, and its mode and route of administration; age, health, and weight of the recipient; nature and extent of symptoms, kind of concurrent treatment,

- 30 -

880 frequency of treatment, and the effect desired. Usually a
daily dosage of active ingredient can be about 0.001 to 1 grams
per kilogram of body weight, in some embodiments about 0.1 to
100 milligrams per kilogram of body weight. Ordinarily dosages
are in the range of 0.5 to 50 milligrams per kilogram of body
weight, and preferably 1 to 10 milligrams per kilogram per day.
885 In some embodiments, the pharmaceutical compositions are given
in divided doses 1 to 6 times a day or in sustained release
form is effective to obtain desired results.

Dosage forms (composition) suitable for internal
administration generally contain from about 1 milligram to
890 about 500 milligrams of active ingredient per unit. In these
pharmaceutical compositions the active ingredient will
ordinarily be present in an amount of about 0.5-95 by weight
based on the total weight of the composition.

Because conjugated compounds are specifically targeted
895 to cells with p185, conjugated compounds which comprise
chemotherapeutics or toxins are administered in doses less than
those which are used when the chemotherapeutics or toxins are
administered as unconjugated active agents, preferably in doses
that contain up to 100 times less active agent. In some
900 embodiments, conjugated compounds which comprise
chemotherapeutics or toxins are administered in doses that
contain 10-100 times less active agent as an active agent than
the dosage of chemotherapeutics or toxins administered as
unconjugated active agents. To determine the appropriate dose,
905 the amount of compound is preferably measured in moles instead
of by weight. In that way, the variable weight of different
compounds of the invention does not affect the calculation.
Presuming a one to one ratio of p185-binding compound to active
agent in conjugated compositions of the invention, less moles
910 of conjugated compounds may be administered as compared to the
moles of unconjugated compounds administered, preferably up to
100 times less moles.

For parenteral administration, the compound can be
formulated as a solution, suspension, emulsion or lyophilized
915 powder in association with a pharmaceutically acceptable

- 31 -

parenteral vehicle. Examples of such vehicles are water, saline, Ringer's solution, dextrose solution, and 5% human serum albumin. Liposomes and nonaqueous vehicles such as fixed oils may also be used. The vehicle or lyophilized powder may contain additives that maintain isotonicity (e.g., sodium chloride, mannitol) and chemical stability (e.g., buffers and preservatives). The formulation is sterilized by commonly used techniques.

Suitable pharmaceutical carriers are described in the most recent edition of *Remington's Pharmaceutical Sciences*, A. Osol, a standard reference text in this field.

For example, a parenteral composition suitable for administration by injection is prepared by dissolving 1.5% by weight of active ingredient in 0.9% sodium chloride solution.

According to the present invention, the compound may be administered to tissue of an individual by topically or by lavage. The compounds may be formulated as a cream, ointment, salve, douche, suppository or solution for topical administration or irrigation. Formulations for such routes administration of pharmaceutical compositions are well known.

Generally, additives for isotonicity can include sodium chloride, dextrose, mannitol, sorbitol and lactose. In some cases, isotonic solutions such as phosphate buffered saline are used. Stabilizers include gelatin and albumin. In some embodiments, a vasoconstriction agent is added to the formulation. The pharmaceutical preparations according to the present invention are preferably provided sterile and pyrogen free.

One of skill in the art of pharmaceutical formulations, e.g., having an advanced degree in Pharmaceutics or Pharmaceutical Sciences, can prepare a variety of appropriate dosage forms and formulations for the compositions of the invention with no more than routine experimentation. A number of texts in the field, a.g., *Remington's Pharmaceutical Sciences* and *The U.S. Pharmacopoeia/National Formulary*, latest editions, provide considerable guidance in this respect.

- 32 -

955 A pharmaceutically acceptable formulation will provide the active ingredient(s) in proper physical form together with such excipients, diluents, stabilizers, preservatives and other ingredients as are appropriate to the nature and composition of the dosage form and the properties of the drug ingredient(s) in the formulation environment and drug delivery system.

960 The compositions may include additional components to render them more effective. For example, a composition of the invention may comprise multiple anti-p185 compounds. The compositions may include other anti-cancer agents such as, for example, cis-platin, methotrexate, and/or G-MCSF. Such compositions would be particularly useful for administration to patients diagnosed and treated for erbB-2-associated cancer.

965 *Administration regimen*

About 5 μ g to 5000 mg of peptide may be administered. In some preferred embodiments, 50 μ g to 500 mg of peptide may be administered. In other preferred embodiments, 500 μ g to 50 mg of peptide may be administered. In a preferred embodiment, 5 mg of peptide is administered.

970 Prophylactic compositions may be administered by an appropriate route such as, for example, by oral, intranasal, intramuscular, intraperitoneal or subcutaneous administration. In some embodiments, intravenous administration is preferred.

975 Subsequent to initial administration, individuals may be boosted by readministration. In some preferred embodiments, multiple administrations are performed.

- 33 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Greene, Mark I.
Zhang, Xin
- (ii) TITLE OF INVENTION: COMPOUNDS THAT BIND TO p185 AND
METHODS OF USING THE SAME
- (iii) NUMBER OF SEQUENCES: 184
- (iv) CORRESPONDENCE ADDRESS:
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 - (B) STREET: One Liberty Place - 46th Floor
 - (C) CITY: Philadelphia
 - (D) STATE: PA
 - (E) COUNTRY: USA
 - (F) ZIP: 19103
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: DISKETTE, 3.5 INCH
 - (B) COMPUTER: IBM PC Compatible
 - (C) OPERATING SYSTEM: PC-DOS
 - (D) SOFTWARE: WORDPERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/433,318
 - (B) FILING DATE: 03-MAY-1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Mark DeLuca
 - (B) REGISTRATION NUMBER: 33,229
 - (C) REFERENCE/DOCKET NUMBER: UPN-2748
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 - (B) TELEFAX: (215) 568-3439

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Phe Lys Thr Asn Lys
1 5

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Asn Trp Asp Trp Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

- 34 -

Asp Asn Trp Asp Trp Tyr
1 5

- (2) INFORMATION FOR SEQ ID NO:4:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Gln Trp Asp Trp Tyr
1 5

- (2) INFORMATION FOR SEQ ID NO:5:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Gln Trp Asp Trp Tyr
1 5

- (2) INFORMATION FOR SEQ ID NO:6:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Asn Trp Glu Trp Tyr
1 5

- (2) INFORMATION FOR SEQ ID NO:7:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Asn Trp Glu Trp Tyr
1 5

- (2) INFORMATION FOR SEQ ID NO:8:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu Gln Trp Glu Trp Tyr
1 5

- (2) INFORMATION FOR SEQ ID NO:9:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6

- 35 -

- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Gln Trp Glu Trp Tyr
1 5

- (2) INFORMATION FOR SEQ ID NO:10:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Glu Asn Trp Asp Trp Phe
1 5

- (2) INFORMATION FOR SEQ ID NO:11:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Asp Asn Trp Asp Trp Phe
1 5

- (2) INFORMATION FOR SEQ ID NO:12:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Glu Gln Trp Asp Trp Phe
1 5

- (2) INFORMATION FOR SEQ ID NO:13:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Gln Trp Asp Trp Phe
1 5

- (2) INFORMATION FOR SEQ ID NO:14:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Asn Trp Glu Trp Phe
1 5

- 36 -

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Asp Asn Trp Glu Trp Phe
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Gln Trp Glu Trp Phe
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Asp Gln Trp Glu Trp Phe
1 5

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 1

(D) OTHER INFORMATION: /note= "Xaa at position 1 is Gly,
Val, Ala, Ile or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 2

(D) OTHER INFORMATION: /note= "Xaa at position 2 is Asp or Glu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 3

(D) OTHER INFORMATION: /note= "Xaa at position 3 is Gly,
Val, Ala, Ile or Leu"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 4

(D) OTHER INFORMATION: /note= "Xaa at position 4 is Phe or Tyr"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 5

(D) OTHER INFORMATION: /note= "Xaa at position 5 is Tyr or Phe"

(ix) FEATURE:

(A) NAME/KEY: Modified-site

- 37 -

(B) LOCATION: 6

(D) OTHER INFORMATION: /note= "Xaa at position 6 is Ala, Gly, Val, Ile or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Xaa Xaa Xaa Xaa Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gly Asp Gly Phe Tyr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Gly Glu Gly Phe Tyr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly Asp Gly Tyr Tyr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Gly Glu Gly Tyr Tyr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Gly Asp Gly Phe Phe Ala

- 38 -

1

5

- (2) INFORMATION FOR SEQ ID NO:24:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Gly Glu Gly Phe Phe Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:25:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gly Asp Gly Tyr Phe Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:26:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Gly Glu Gly Tyr Phe Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:27:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ala Asp Gly Phe Tyr Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:28:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ala Glu Gly Phe Tyr Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:29:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid

- 39 -

- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ala Asp Gly Tyr Tyr Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:30:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Ala Glu Gly Tyr Tyr Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:31:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Ala Asp Gly Phe Phe Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:32:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ala Glu Gly Phe Phe Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:33:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ala Asp Gly Tyr Phe Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:34:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Ala Glu Gly Tyr Phe Ala
1 5

- 40 -

- (2) INFORMATION FOR SEQ ID NO:35:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gly Asp Ala Phe Tyr Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:36:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Glu Ala Phe Tyr Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:37:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gly Asp Ala Tyr Tyr Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:38:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Glu Ala Tyr Tyr Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:39:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Gly Asp Ala Phe Phe Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:40:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

- 41 -

Gly Glu Ala Phe Phe Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:41:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Gly Asp Ala Tyr Phe Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:42:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gly Glu Ala Tyr Phe Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:43:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ala Asp Ala Phe Tyr Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:44:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Ala Glu Ala Phe Tyr Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:45:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ala Asp Ala Tyr Tyr Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:46:
(i) SEQUENCE CHARACTERISTICS:

- 42 -

- (A) LENGTH: 6
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Ala Glu Ala Tyr Tyr Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:47:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Ala Asp Ala Phe Phe Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:48:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Ala Glu Ala Phe Phe Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:49:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Ala Asp Ala Tyr Phe Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:50:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Ala Glu Ala Tyr Phe Ala
1 5

- (2) INFORMATION FOR SEQ ID NO:51:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Gly Asp Gly Phe Tyr Gly

- 43 -

1

5

- (2) INFORMATION FOR SEQ ID NO:52:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gly Glu Gly Phe Tyr Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:53:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Gly Asp Gly Tyr Tyr Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:54:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Glu Gly Tyr Tyr Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:55:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gly Asp Gly Phe Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:56:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Gly Glu Gly Phe Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:57:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid

- 44 -

- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Gly Asp Gly Tyr Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:58:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Gly Glu Gly Tyr Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:59:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Asp Gly Phe Tyr Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:60:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Ala Glu Gly Phe Tyr Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:61:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Asp Gly Tyr Tyr Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:62:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Ala Glu Gly Tyr Tyr Gly
1 5

- 45 -

- (2) INFORMATION FOR SEQ ID NO:63:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ala Asp Gly Phe Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:64:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ala Glu Gly Phe Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:65:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Ala Asp Gly Tyr Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:66:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ala Glu Gly Tyr Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:67:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Gly Asp Ala Phe Tyr Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:68:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
 (ii) MOLECULE TYPE: peptide
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

- 46 -

Gly Glu Ala Phe Tyr Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:69:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Gly Asp Ala Tyr Tyr Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:70:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Gly Glu Ala Tyr Tyr Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:71:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Gly Asp Ala Phe Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:72:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Gly Glu Ala Phe Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:73:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Asp Ala Tyr Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:74:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6

- 47 -

- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gly Glu Ala Tyr Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:75:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ala Asp Ala Phe Tyr Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:76:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Ala Glu Ala Phe Tyr Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:77:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ala Asp Ala Tyr Tyr Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:78:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ala Glu Ala Tyr Tyr Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:79:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ala Asp Ala Phe Phe Gly
1 5

- 48 -

- (2) INFORMATION FOR SEQ ID NO:80:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ala Glu Ala Phe Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:81:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Ala Asp Ala Tyr Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:82:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Ala Glu Ala Tyr Phe Gly
1 5

- (2) INFORMATION FOR SEQ ID NO:83:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Tyr Pro Pro Gly Cys
1 5

- (2) INFORMATION FOR SEQ ID NO:84:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Tyr Met Asp Val
1

- (2) INFORMATION FOR SEQ ID NO:85:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide

- 49 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Phe	Glu	Cys	Glu	Asn	Trp	Asp	Trp	Tyr	Cys	Tyr	Pro	Pro	Gly	Cys
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Phe	Cys	Gly	Asp	Gly	Phe	Tyr	Ala	Cys	Met	Asp	Val
1				5						10	

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Phe	Glu	Cys	Asp	Asn	Trp	Asp	Trp	Tyr	Cys	Tyr	Pro	Pro	Gly	Cys
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Phe	Glu	Cys	Glu	Gln	Trp	Asp	Trp	Tyr	Cys	Tyr	Pro	Pro	Gly	Cys
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Phe	Glu	Cys	Asp	Gln	Trp	Asp	Trp	Tyr	Cys	Tyr	Pro	Pro	Gly	Cys
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Phe	Glu	Cys	Glu	Asn	Trp	Glu	Trp	Tyr	Cys	Tyr	Pro	Pro	Gly	Cys
1				5					10					15

(2) INFORMATION FOR SEQ ID NO:91:

- 50 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Phe Glu Cys Asp Asn Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:92:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Phe Glu Cys Glu Gln Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:93:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Phe Glu Cys Asp Gln Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:94:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Phe Glu Cys Glu Asn Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:95:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Phe Glu Cys Asp Asn Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:96:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

- 51 -

Phe Glu Cys Glu Gln Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Phe Glu Cys Asp Gln Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Phe Glu Cys Glu Asn Trp Glu Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Phe Glu Cys Asp Asn Trp Glu Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Phe Glu Cys Glu Gln Trp Glu Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Phe Glu Cys Asp Gln Trp Glu Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

- 52 -

- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

Phe Cys Glu Asn Trp Asp Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

- (2) INFORMATION FOR SEQ ID NO:103:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Phe Cys Asp Asn Trp Asp Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

- (2) INFORMATION FOR SEQ ID NO:104:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Phe Cys Glu Gln Trp Asp Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

- (2) INFORMATION FOR SEQ ID NO:105:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Phe Cys Asp Gln Trp Asp Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

- (2) INFORMATION FOR SEQ ID NO:106:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Phe Cys Glu Asn Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

- (2) INFORMATION FOR SEQ ID NO:107:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Phe Cys Asp Asn Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

- 53 -

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Phe Cys Glu Gln Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Phe Cys Asp Gln Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Phe Cys Glu Asn Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Phe Cys Asp Asn Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Phe Cys Glu Gln Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

- 54 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Phe	Cys	Asp	Gln	Trp	Asp	Trp	Phe	Cys	Tyr	Pro	Pro	Gly	Cys
1				5					10				

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Phe	Cys	Glu	Asn	Trp	Glu	Trp	Phe	Cys	Tyr	Pro	Pro	Gly	Cys
1				5					10				

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Phe	Cys	Asp	Asn	Trp	Glu	Trp	Phe	Cys	Tyr	Pro	Pro	Gly	Cys
1				5					10				

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Phe	Cys	Glu	Gln	Trp	Glu	Trp	Phe	Cys	Tyr	Pro	Pro	Gly	Cys
1				5					10				

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Phe	Cys	Asp	Gln	Trp	Glu	Trp	Phe	Cys	Tyr	Pro	Pro	Gly	Cys
1				5					10				

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Phe	Glu	Cys	Glu	Asn	Trp	Asp	Trp	Tyr	Cys	Tyr
1				5				10		

(2) INFORMATION FOR SEQ ID NO:119:

- 55 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Phe Glu Cys Asp Asn Trp Asp Trp Tyr Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:120:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Phe Glu Cys Glu Gln Trp Asp Trp Tyr Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:121:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Phe Glu Cys Asp Gln Trp Asp Trp Tyr Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:122:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Phe Glu Cys Glu Asn Trp Glu Trp Tyr Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:123:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Phe Glu Cys Asp Asn Trp Glu Trp Tyr Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:124:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

- 56 -

Phe Glu Cys Glu Gln Trp Glu Trp Tyr Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:125:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Phe Glu Cys Asp Gln Trp Glu Trp Tyr Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:126:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Phe Glu Cys Glu Asn Trp Asp Trp Phe Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:127:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Phe Glu Cys Asp Asn Trp Asp Trp Phe Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:128:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Phe Glu Cys Glu Gln Trp Asp Trp Phe Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:129:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11
(B) TYPE: amino acid
(D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Phe Glu Cys Asp Gln Trp Asp Trp Phe Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:130:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11

- 57 -

- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Phe Glu Cys Glu Asn Trp Glu Trp Phe Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:131:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Phe Glu Cys Asp Asn Trp Glu Trp Phe Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:132:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Phe Glu Cys Glu Gln Trp Glu Trp Phe Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:133:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Phe Glu Cys Asp Gln Trp Glu Trp Phe Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:134:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Phe Cys Glu Asn Trp Asp Trp Tyr Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:135:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Phe Cys Asp Asn Trp Asp Trp Tyr Cys Tyr
1 5 10

- 58 -

- (2) INFORMATION FOR SEQ ID NO:136:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Phe Cys Glu Gln Trp Asp Trp Tyr Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:137:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Phe Cys Asp Gln Trp Asp Trp Tyr Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:138:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

Phe Cys Glu Asn Trp Glu Trp Tyr Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:139:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Phe Cys Asp Asn Trp Glu Trp Tyr Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:140:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Phe Cys Glu Gln Trp Glu Trp Tyr Cys Tyr
1 5 10

- (2) INFORMATION FOR SEQ ID NO:141:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide

- 59 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Phe Cys Asp Gln Trp Glu Trp Tyr Cys Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Phe Cys Glu Asn Trp Asp Trp Phe Cys Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Phe Cys Asp Asn Trp Asp Trp Phe Cys Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Phe Cys Glu Gln Trp Asp Trp Phe Cys Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Phe Cys Asp Gln Trp Asp Trp Phe Cys Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Phe Cys Glu Asn Trp Glu Trp Phe Cys Tyr
1 5 10

(2) INFORMATION FOR SEQ ID NO:147:

- 60 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Phe Cys Asp Asn Trp Glu Trp Phe Cys Tyr
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:148:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Phe Cys Glu Gln Trp Glu Trp Phe Cys Tyr
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:149:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Phe Cys Asp Gln Trp Glu Trp Phe Cys Tyr
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:150:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

Phe Glu Cys Asp Asn Trp Asp Trp Tyr Cys Tyr Pro Pro Gly Cys
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:151:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Phe Glu Cys Glu Gln Trp Asp Trp Tyr Cys Tyr Pro Pro Gly Cys
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:152:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

- 61 -

Phe Glu Cys Asp Gln Trp Asp Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Phe Glu Cys Glu Asn Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Phe Glu Cys Asp Asn Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

Phe Glu Cys Glu Gln Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Phe Glu Cys Asp Gln Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Phe Glu Cys Glu Asn Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

- 62 -

- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Phe Glu Cys Asp Asn Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:159:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Phe Glu Cys Glu Gln Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:160:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Phe Glu Cys Asp Gln Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:161:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

Phe Glu Cys Glu Asn Trp Glu Trp Phe Cys Tyr Pro Pro Gly Cys
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:162:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Phe Glu Cys Asp Asn Trp Glu Trp Phe Cys Tyr Pro Pro Gly Cys
 1 5 10 15

- (2) INFORMATION FOR SEQ ID NO:163:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Phe Glu Cys Glu Gln Trp Glu Trp Phe Cys Tyr Pro Pro Gly Cys
 1 5 10 15

- 63 -

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Phe Glu Cys Asp Gln Trp Glu Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Phe Cys Glu Asn Trp Asp Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Phe Cys Asp Asn Trp Asp Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

Phe Cys Glu Gln Trp Asp Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Phe Cys Asp Gln Trp Asp Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

- 64 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Phe Cys Glu Asn Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Phe Cys Asp Asn Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Phe Cys Glu Gln Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Phe Cys Asp Gln Trp Glu Trp Tyr Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Phe Cys Glu Asn Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14
(B) TYPE: amino acid
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

Phe Cys Asp Asn Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO:175:

- 65 -

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Phe Cys Glu Gln Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10

- (2) INFORMATION FOR SEQ ID NO:176:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Phe Cys Asp Gln Trp Asp Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10

- (2) INFORMATION FOR SEQ ID NO:177:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Phe Cys Glu Asn Trp Glu Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10

- (2) INFORMATION FOR SEQ ID NO:178:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Phe Cys Asp Asn Trp Glu Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10

- (2) INFORMATION FOR SEQ ID NO:179:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Phe Cys Glu Gln Trp Glu Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10

- (2) INFORMATION FOR SEQ ID NO:180:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: unknown
 - (ii) MOLECULE TYPE: peptide
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

- 66 -

Phe Cys Asp Gln Trp Glu Trp Phe Cys Tyr Pro Pro Gly Cys
1 5 10

- (2) INFORMATION FOR SEQ ID NO:181:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Cys Tyr Pro Pro Gly Cys
1 5

- (2) INFORMATION FOR SEQ ID NO:182:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Cys Tyr Met Asp Val
1 5

- (2) INFORMATION FOR SEQ ID NO:183:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Cys Phe Asp Val
1

- (2) INFORMATION FOR SEQ ID NO:184:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13
 (B) TYPE: amino acid
 (D) TOPOLOGY: unknown
(ii) MOLECULE TYPE: peptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Phe Cys Gly Asp Gly Phe Tyr Ala Cys Tyr Met Asp Val
1 5 10

- 67 -

CLAIMS

1. A peptide having the formula:



wherein:

5 R_1 is 1-6 amino acid residues and at least one of which is tyrosine or phenylalanine;

R_2 is a linking moiety which bonds with R_1 , R_3 and R_6 such that a portion of said peptide is cyclicized;

R_3 is 0-20 amino acids;

10 R_4 is 6 amino acids;

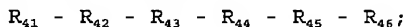
R_5 is 0-20 amino acids;

R_6 is a linking moiety which bonds with R_5 , R_7 and R_2 such that a portion of said peptide is cyclicized;

15 R_7 is 1-6 amino acid residues and at least one of which is tyrosine or phenylalanine;

wherein: R_1 , R_2 , R_3 , R_4 , R_5 , R_6 and R_7 , taken together, are 30 amino acids or less;

and R_4 has the formula:



20 wherein:

either,

R_{41} is Glu or Asp;

R_{42} is Asn or Gln;

R_{43} is Trp;

25 R_{44} is Asp or Glu;

R_{45} is Trp; and,

R_{46} is Tyr or Phe;

or

R_{41} is Gly, Val, Ala, Ile or Leu;

30 R_{42} is Asp or Glu;

R_{43} is Gly, Val, Ala, Ile or Leu;

R_{44} is Phe or Tyr;

R_{45} is Tyr or Phe; and,

R_{46} is Ala, Ile, Leu, Gly or Val.

35 2. The peptide of claim 1 wherein R_1 comprises of Phe-Glu, Tyr-Glu, Phe or Tyr.

- 68 -

3. The peptide of claim 1 wherein R_1 consists of Phe-Glu, Tyr-Glu, Phe or Tyr.
4. The peptide of claim 1 wherein R_2 is cysteine and R_5 is cysteine.
- 5 5. The peptide of claim 1 wherein R_3 is 0 amino acids.
6. The peptide of claim 1 wherein R_4 is selected from the group consisting of SEQ ID NOS:2-17.
7. The peptide of claim 1 wherein R_4 is SEQ ID NO:18.
8. The peptide of claim 1 wherein R_4 is selected from the
10 group consisting of SEQ ID NOS:19-82.
9. The peptide of claim 1 wherein R_5 is 0 amino acids.
10. The peptide of claim 1 wherein R_5 comprises of Phe, Tyr, SEQ ID NO:83, SEQ ID NO:84 or Phe-Asp-Val.
11. The peptide of claim 1 wherein R_1 consists of Phe,
15 Tyr, SEQ ID NO:83, SEQ ID NO:84 or Phe-Asp-Val.
12. The peptide of claim 1 wherein R_1 , R_2 , R_3 , R_4 , R_5 , R_6 and R_7 , taken together, are less than 20 amino acids.
13. The peptide of claim 1 wherein said peptide has an amino acid sequence selected from the group consisting of SEQ
20 ID NOS:85-180.
14. The peptide of claim 1 wherein said peptide comprises an amino acid sequence SEQ ID NO:181.
15. The peptide of claim 1 wherein:
 R_1 - R_2 - R_3 is Phe-Cys, Tyr-Cys, Phe-Glu-Cys, or Tyr-Glu-
25 Cys;

- 69 -

R₄ is SEQ ID NO:18; and

R₅ -R₆ -R₇ is SEQ ID NO:181, SEQ ID NO:182, Cys-Phe, SEQ ID NO:183 or Cys-Tyr.

16. The peptide of claim 1 wherein:

5 R₁-R₂-R₃ is Phe-Cys, Tyr-Cys, Phe-Glu-Cys, or Tyr-Glu-Cys;
R₄ is selected from the group SEQ ID NOs:19-82; and

R₅ -R₆ -R₇ is SEQ ID NO:181, SEQ ID NO:182), Cys-Phe, SEQ ID NO:183 or Cys-Tyr.

17. The peptide of claim 1 having the amino acid sequence
10 F-C-G-D-G-F-Y-A-C-Y-M-D-V (SEQ ID NO:184).

18. A conjugated composition comprising a peptide according to claim 1 linked to a detectable agent and/or cytotoxic agent.

19. The conjugated composition of claim 18 wherein said
15 peptide is linked to a detectable agent, said detectable agent is a radioisotope.

20. A method of detecting a tumor that has p185 on tumor cell surfaces comprising the step of administering, to an individual suspected of having such a tumor or being
20 susceptible to such a tumor, a conjugated composition according to claim 19 and detecting the presence of localized conjugated composition within the body of said individual.

21. The conjugated composition of claim 18 wherein said peptide is linked to a cytotoxic agent selected from the group
25 consisting of: cytotoxic drugs, toxins and cytostatic drugs.

22. A pharmaceutical composition comprising
a peptide according to claim 1, and
a pharmaceutically acceptable carrier or diluent.

- 70 -

23. A method of preventing transformation of a normal cell into a tumor cell in an individual at risk of developing a tumor having tumor cells which have p185 on their surfaces, said method comprising the steps of:

- 5 a) identifying said individual; and,
 b) administering to said individual a compound according to claim 1.

24. A method of treating an individual who has cancer characterized by tumor cells that have a p185 on their cell surfaces comprising the steps of:

- a) identifying said individual;
5 b) administering to said individual, a therapeutically effective amount of a peptide according to claim 1.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/06270

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : A61K 38/02, 38/08; C07K 7/00, 7/02, 14/00
US CL : 514/12, 13, 14, 15; 530/324, 325, 326, 327, 328

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 514/12, 13, 14, 15; 530/324, 325, 326, 327, 328

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, STN
search terms: tumor detection, p185, peptides.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	US 5,367,060 A (VANDLEN ET AL) 22 November 1994 (22/11/94), see entire document.	1-17
A	US 5,464,751 A (GREENE ET AL) 07 November 1995 (07/11/95), see entire document.	1-17
A	US 5,200,178 A (STRAUSS ET AL) 06 April 1993 (06/04/93), see entire document.	18-20
A	ZABRECKY et al. The Extracellular Domain of p185/neu Is Release From the Surface of Human Breast Carcinoma Cells, SK-BR-3. Journal of Biological Chemistry. 25 January 1991, Vol.256, No.3, pages 1716-1720, see entire document.	18-20



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document published on or after the international filing date
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- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T

later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X

document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y

document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

Z

document member of the same patent family

Date of the actual completion of the international search

30 JULY 1996

Date of mailing of the international search report

13 SEP 1996

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/06270

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	BERGE et al. Pharmaceutical Salts. Journal of Pharmaceutical Sciences. January 1977, Vol.66, No.1, pages 1-19, see entire document.	21